



SEQUENCE LISTING

<110> Lanes, Olav
Willasen, Nils Peder
Guddal, Per Henrik
Gjellesvik, Dag Rune

<120> COD URACIL-DNA GLYCOSYLASE, GENE CODING THEREFORE, RECOMBINANT DNA
CONTAINING SAID GENE OR OPERATIVE PARTS THEREOF, A METHOD FOR PREPARING SAID
PROTEIN AND THE USE OF SAID PROTEIN OR SAID OPERATIVE PARTS THEREOF IN
MONITORING OR CONTROLLING PCR

<130> U 013209-3

<140> 09/758,017

<141> 2001-01-10

<150> 2000 5428

<151> 2000-10-27

<150> 2000 0163

<151> 2000-01-12

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 1283

<212> DNA

<213> GADUS MORHUA

<220>

<221> CDS

<222> (18)..(920)

<223>

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Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys
1 5 10

ata tca tca aat cgg gty tta cca ggt tta cta att ccc caa act tta 98
Ile Ser Ser Asn Arg Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu
15 20 25

tgt ttt tct aaa tta atg aag ata acg ccg aag aaa ctg agg tcc tca 146
Cys Phe Ser Lys Leu Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser
30 35 40

aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg gag cag ctg 194
Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu
45 50 55

gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag att aga gca 242
Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala
60 65 70 75

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TECH CENTER 1600/2900

C4

aaa gca acg cct gca ggt ttc gga gag act tgg aga aga gag ctg gct	290
Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala	
80 85 90	
gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc ttt gta gct	338
Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala	
95 100 105	
gat gag agg agc cgt cac acc gtc tac cca ccg gct gat caa gtg tac	386
Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr	
110 115 120	
agt tgg aca gag atg tgt gac att caa gat gtg aaa gta gtg att cta	434
Ser Trp Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu	
125 130 135	
ggc cag gac cct tac cac ggt ccc aac caa gca cat gga ctc tgt ttc	482
Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly Leu Cys Phe	
140 145 150 155	
agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg aac ata tac	530
Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr	
160 165 170	
aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct gga cat gga	578
Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro Gly His Gly	
175 180 185	
gat cta agc gga tgg gca aaa caa ggg gtg ctg ctg ctt aac gcg gtg	626
Asp Leu Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val	
190 195 200	
ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac aga ggc tgg	674
Leu Thr Val Arg Ala His Gln Ala Asn Ser His Lys Asp Arg Gly Trp	
205 210 215	
gag acc ttc acc gac gct gtg atc aag tgg ctg agc gtc aac cgg gaa	722
Glu Thr Phe Thr Asp Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu	
220 225 230 235	
gga gtg gtt ttc ctg ttg tgg ggc tca tac gcc cat aag aag gga gcg	770
Gly Val Val Phe Leu Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala	
240 245 250	
acc atc gac agg aaa cgt cac cat gtc ttg caa gct gtt cat cca tct	818
Thr Ile Asp Arg Lys Arg His His Val Leu Gln Ala Val His Pro Ser	
255 260 265	
cct ttg tct gct cat cgt ggg ttc ctt ggt tgt aag cac ttc tcc aag	866
Pro Leu Ser Ala His Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys	
270 275 280	
gct aac ggg ctg ctg aaa cta tct ggg acg gag cct ata aac tgg aga	914
Ala Asn Gly Leu Leu Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg	
285 290 295	

gca ctc taactcttta tgctgcctta tactgttaac tgttttaaga tgaacatcac 970
 Ala Leu
 300

actatatattt ctacagcttt tccaagttca aaccaatcta taagctttca tttgtctttt 1030
 ggaatgatgc tgcttttggt cggttttaga tacttaaaac actttaccac tctgccatgt 1090
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 <213> GADUS MORHUA

<220>
 <221> misc_feature
 <222> (17)..(17)
 <223> The 'Xaa' at location 17 stands for Val.

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Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
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Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
 35 40 45

Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
 50 55 60

Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
 65 70 75 80

Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
 85 90 95

Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
 100 105 110

His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met
 115 120 125

Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
 130 135 140

His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
 145 150 155 160

Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
 165 170 175

Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
 180 185 190

Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala
 195 200 205

His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp
 210 215 220

Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
 225 230 235 240

Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
 245 250 255

Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His
 260 265 270

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 275 280 285

Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
 290 295 300

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 <212> DNA
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<220>
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 <222> (90) .. (992)
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Met Ile Gly Gln Gln His Ile Asn
1 5
tct ttc ttc tca cca gtt tca aaa aag aga gtt tca aag gaa tta ggt 161
Ser Phe Phe Ser Pro Val Ser Lys Lys Arg Val Ser Lys Glu Leu Gly
10 15 20
aaa acc gaa aag cat gcc gaa gaa gtt cag ata acg ccg aag aaa ctg 209
Lys Thr Glu Lys His Ala Glu Glu Val Gln Ile Thr Pro Lys Lys Leu
25 30 35 40
agg tcc tca aat gtg gaa caa aag acg tca tcg cca cag ctt tca gtg 257
Arg Ser Ser Asn Val Glu Gln Lys Thr Ser Ser Pro Gln Leu Ser Val
45 50 55
gag cag ctg gaa aga atg gcc aaa aat aag aaa gca gcg ctt gac aag 305
Glu Gln Leu Glu Arg Met Ala Lys Asn Lys Lys Ala Ala Leu Asp Lys
60 65 70
att aga gca aaa gca acg cct gca ggt ttc gga gag act tgg aga aga 353
Ile Arg Ala Lys Ala Thr Pro Ala Gly Phe Gly Glu Thr Trp Arg Arg
75 80 85
gag ctg gct gca gag ttt gaa aag cca tac ttc aaa caa ttg atg tcc 401
Glu Leu Ala Ala Glu Phe Glu Lys Pro Tyr Phe Lys Gln Leu Met Ser
90 95 100
ttt gta gct gat gag agg agc cgt cac acc gtc tac cca ccg gct gat 449
Phe Val Ala Asp Glu Arg Ser Arg His Thr Val Tyr Pro Pro Ala Asp
105 110 115 120
caa gtg tac agt tgg aca gag atg tgt gac att caa gat gtg aaa gta 497
Gln Val Tyr Ser Trp Thr Glu Met Cys Asp Ile Gln Asp Val Lys Val
125 130 135
gtg att cta ggc cag gac cct tac cac ggt ccc aac caa gca cat gga 545
Val Ile Leu Gly Gln Asp Pro Tyr His Gly Pro Asn Gln Ala His Gly
140 145 150
ctc tgt ttc agt gtg caa aag cca gtt ccc cct ccc ccc agt ctc gtg 593
Leu Cys Phe Ser Val Gln Lys Pro Val Pro Pro Pro Pro Ser Leu Val
155 160 165
aac ata tac aaa gaa ttg tgt acc gac att gat ggc ttc aag cat cct 641
Asn Ile Tyr Lys Glu Leu Cys Thr Asp Ile Asp Gly Phe Lys His Pro
170 175 180
gga cat gga gat cta agc gga tgg gca aaa caa ggg gtg ctg ctg ctt 689
Gly His Gly Asp Leu Ser Gly Trp Ala Lys Gln Gly Val Leu Leu Leu
185 190 195 200
aac gcg gtg ctg acc gtg cgg gcc cat cag gcc aac tcc cac aag gac 737

Asn	Ala	Val	Leu	Thr	Val	Arg	Ala	His	Gln	Ala	Asn	Ser	His	Lys	Asp																						
				205					210					215																							
aga	ggc	tgg	gag	acc	ttc	acc	gac	gct	gtg	atc	aag	tgg	ctg	agc	gtc	785																					
Arg	Gly	Trp	Glu	Thr	Phe	Thr	Asp	Ala	Val	Ile	Lys	Trp	Leu	Ser	Val																						
			220					225					230																								
aac	cgg	gaa	gga	gtg	gtt	ttc	ctg	ttg	tgg	ggc	tca	tac	gcc	cat	aag	833																					
Asn	Arg	Glu	Gly	Val	Val	Phe	Leu	Leu	Trp	Gly	Ser	Tyr	Ala	His	Lys																						
		235					240					245																									
aag	gga	gcg	acc	atc	gac	agg	aaa	cgt	cac	cat	gtc	ttg	caa	gct	gtt	881																					
Lys	Gly	Ala	Thr	Ile	Asp	Arg	Lys	Arg	His	His	Val	Leu	Gln	Ala	Val																						
	250					255					260																										
cat	cca	tct	cct	ttg	tct	gct	cat	cgt	ggg	ttc	ctt	ggg	tgt	aag	cac	929																					
His	Pro	Ser	Pro	Leu	Ser	Ala	His	Arg	Gly	Phe	Leu	Gly	Cys	Lys	His																						
265					270					275					280																						
ttc	tcc	aag	gct	aac	ggg	ctg	ctg	aaa	cta	tct	ggg	acg	gag	cct	ata	977																					
Phe	Ser	Lys	Ala	Asn	Gly	Leu	Leu	Lys	Leu	Ser	Gly	Thr	Glu	Pro	Ile																						
				285					290					295																							
aac	tgg	aga	gca	ctc	taactcttta tgctgcctta tactgttaac tgttttaaga											1032																					
Asn	Trp	Arg	Ala	Leu																																	
			300																																		
tga	acatcac	actatatatttt				ctacagcttt			tccaagttca			aaccaatcta			taagctttca		1092																				
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tgc	agaaata	aattatatat				tta											1355																				

Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
50 55 60

Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
65 70 75 80

Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
85 90 95

Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
100 105 110

His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Trp Thr Glu Met
115 120 125

Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
130 135 140

His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
145 150 155 160

Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr
165 170 175

Asp Ile Asp Gly Phe Lys His Pro Gly His Gly Asp Leu Ser Gly Trp
180 185 190

Ala Lys Gln Gly Val Leu Leu Leu Asn Ala Val Leu Thr Val Arg Ala
195 200 205

His Gln Ala Asn Ser His Lys Asp Arg Gly Trp Glu Thr Phe Thr Asp
210 215 220

Ala Val Ile Lys Trp Leu Ser Val Asn Arg Glu Gly Val Val Phe Leu
225 230 235 240

Leu Trp Gly Ser Tyr Ala His Lys Lys Gly Ala Thr Ile Asp Arg Lys
245 250 255

Arg His His Val Leu Gln Ala Val His Pro Ser Pro Leu Ser Ala His
260 265 270

Arg Gly Phe Leu Gly Cys Lys His Phe Ser Lys Ala Asn Gly Leu Leu
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Lys Leu Ser Gly Thr Glu Pro Ile Asn Trp Arg Ala Leu
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<210> 5
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<212> PRT
<213> GADUS MORHUA

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<400> 6

Ala Leu Leu Gln Gly
1 5

<210> 7
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<212> PRT
<213> GADUS MORHUA

<400> 7

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<210> 8
<211> 27
<212> DNA
<213> ARTIFICIAL SEQUENCE

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<223> Artificial Sequence - Primer used to generate cDNA of a fragment
of UNG gene

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<210> 12
<211> 27
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<210> 13
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<213> ARTIFICIAL SEQUENCE

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27

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<212> DNA

<213> Artificial

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28

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<213> ARTIFICIAL SEQUENCE

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<213> ARTIFICIAL SEQUENCE

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<210> 17

<211> 37

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<220>

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